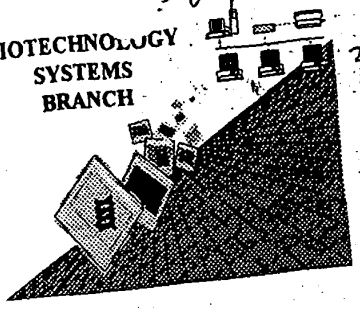
0400 1700 0280 3/6/1 0590 10/05

BIOTECHNOLOGY SYSTEMS BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/757,415

Source: OIPE

Date Processed by STIC: 1/25/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION SERIAL NUMBER: 09/757,415

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____	Wrapped Nucleics	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".
2 ____	Wrapped Aminos	The amino acid number/text at the end of each line "wrapped " down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".
3 ____	Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces.
4 ____	Misaligned Amino Acid Numbering	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
5 ____	Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
6 ____	Variable Length	Sequence(s) ____ contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
7 ____	PatentIn ver. 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
8 ____	Skipped Sequences (OLD RULES)	Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS") (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: This sequence is intentionally skipped Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
9 ____	Skipped Sequences (NEW RULES)	Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence. <210> sequence id number <400> sequence id number 000
10 ____	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
11 ____	Use of <213>Organism (NEW RULES)	Sequence(s) _____ are missing this mandatory field or its response.
12 ____	Use of <220>Feature (NEW RULES)	Sequence(s) ____ are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown" **Please explain source of genetic material in <220> to <223> section.** (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
13 ____	PatentIn ver. 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING DATE: 01/25/2001
PATENT APPLICATION: US/09/757,415 TIME: 11:32:38

Input Set : A:\2459002n.app
Output Set: N:\CRF3\01252001\I757415.raw

Does Not Comply
Corrected Diskette Needed

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 3 <110> APPLICANT: Zhou, Ming-Ming
 5 <120> TITLE OF INVENTION: METHODS OF IDENTIFYING MODULATORS OF THE FGF RECEPTOR
 7 <130> FILE REFERENCE: 2459-1-002N
 9 <140> CURRENT APPLICATION NUMBER: US/09/757,415
10 <141> CURRENT FILING DATE: 2001-01-09
12 <150> PRIOR APPLICATION NUMBER: 60/175,867
13 <151> PRIOR FILING DATE: 2000-01-12
15 <160> NUMBER OF SEQ ID NOS: 7
17 <170> SOFTWARE: PatentIn Ver. 2.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 508
21 <212> TYPE: PRT
22 <213> ORGANISM: Homo sapien
24 <400> SEQUENCE: 1
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28 His Arg Asn Lys Phe Lys Val Ile Asn Val Asp Asp Asp Gly Asn Glu
29              20                  25                  30
31 Leu Gly Ser Gly Ile Met Glu Leu Thr Asp Thr Glu Leu Ile Leu Tyr
32          35                  40                  45
34 Thr Arg Lys Arg Asp Ser Val Lys Trp His Tyr Leu Cys Leu Arg Arg
35      50                  55                  60
37 Tyr Gly Tyr Asp Ser Asn Leu Phe Ser Phe Glu Ser Gly Arg Arg Cys
38  65                  70                  75                  80
40 Gln Thr Gly Gln Gly Ile Phe Ala Phe Lys Cys Ala Arg Ala Glu Glu
41                  85                  90                  95
43 Leu Phe Asn Met Leu Gln Glu Ile Met Gln Asn Asn Ser Ile Asn Val
44             100                 105                 110
46 Val Glu Glu Pro Val Val Glu Arg Asn Asn His Gln Thr Glu Leu Glu
47         115                 120                 125
49 Val Pro Arg Thr Pro Arg Thr Pro Thr Thr Pro Gly Phe Ala Ala Gln
50     130                 135                 140
52 Asn Leu Pro Asn Gly Tyr Pro Arg Tyr Pro Ser Phe Gly Asp Ala Ser
53 145                 150                 155                 160
55 Ser His Pro Ser Ser Arg His Pro Ser Val Gly Ser Ala Arg Leu Pro
56                 165                 170                 175
58 Ser Val Gly Glu Glu Ser Thr His Pro Leu Leu Val Ala Glu Glu Gln
59             180                 185                 190
61 Val His Thr Tyr Val Asn Thr Thr Gly Val Gln Glu Glu Arg Lys Asn
62         195                 200                 205
64 Arg Thr Ser Val His Val Pro Leu Glu Ala Arg Val Ser Asn Ala Glu
65     210                 215                 220
67 Ser Ser Thr Pro Lys Glu Glu Pro Ser Ser Ile Glu Asp Arg Asp Pro
68 225                 230                 235                 240
70 Gln Ile Leu Leu Glu Pro Glu Gly Val Lys Phe Val Leu Gly Pro Thr
71                 245                 250                 255
73 Pro Val Gln Lys Gln Leu Met Glu Lys Glu Lys Leu Glu Gln Leu Gly
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RAW SEQUENCE LISTING DATE: 01/25/2001
PATENT APPLICATION: US/09/757,415 TIME: 11:32:38

Input Set : A:\2459002n.app
Output Set: N:\CRF3\01252001\I757415.raw

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74              260                 265                 270
76 Arg Asp Gln Val Ser Gly Ser Gly Ala Asn Asn Thr Glu Trp Asp Thr
77          275                 280                 285
79 Gly Tyr Asp Ser Asp Glu Arg Arg Asp Ala Pro Ser Val Asn Lys Leu
80      290                 295                 300
82 Val Tyr Glu Asn Ile Asn Gly Leu Ser Ile Pro Ser Ala Ser Gly Val
83 305                 310                 315                 320
85 Arg Arg Gly Arg Leu Thr Ser Thr Ser Thr Ser Asp Thr Gln Asn Ile
86                  325                 330                 335
88 Asn Asn Ser Ala Gln Arg Arg Thr Ala Leu Leu Asn Tyr Glu Asn Leu
89              340                 345                 350
91 Pro Ser Leu Pro Pro Val Trp Glu Ala Arg Lys Leu Ser Arg Asp Glu
92          355                 360                 365
94 Asp Asp Asn Leu Gly Pro Lys Thr Pro Ser Leu Asn Gly Tyr His Asn
95      370                 375                 380
97 Asn Leu Asp Pro Met His Asn Tyr Val Asn Thr Glu Asn Val Thr Val
98 385                 390                 395                 400
100 Pro Ala Ser Ala His Lys Ile Glu Tyr Ser Arg Arg Arg Asp Cys Thr
101                 405                 410                 415
103 Pro Thr Val Phe Asn Phe Asp Ile Arg Arg Pro Ser Leu Glu His Arg
104             420                 425                 430
106 Gln Leu Asn Tyr Ile Gln Val Asp Leu Glu Gly Gly Ser Asp Ser Asp
107         435                 440                 445
109 Asn Pro Gln Thr Pro Lys Thr Pro Thr Thr Pro Leu Pro Gln Thr Pro
110     450                 455                 460
112 Thr Arg Arg Thr Glu Leu Tyr Ala Val Ile Asp Ile Glu Arg Thr Ala
113 465                 470                 475                 480
115 Ala Met Ser Asn Leu Gln Lys Ala Leu Pro Arg Asp Asp Gly Thr Ser
116                 485                 490                 495
118 Arg Lys Thr Arg His Asn Ser Thr Asp Leu Pro Met
119             500                 505
122 <210> SEQ ID NO: 2
123 <211> LENGTH: 822
124 <212> TYPE: PRT
125 <213> ORGANISM: Mouse
127 <400> SEQUENCE: 2
128 Met Trp Gly Trp Lys Cys Leu Leu Phe Trp Ala Val Leu Val Thr Ala
129   1               5                  10                  15
131 Thr Leu Cys Thr Ala Arg Pro Ala Pro Thr Leu Pro Glu Gln Ala Gln
132              20                  25                  30
134 Pro Trp Gly Val Pro Val Glu Val Glu Ser Leu Leu Val His Pro Gly
135          35                  40                  45
137 Asp Leu Leu Gln Leu Arg Cys Arg Leu Arg Asp Asp Val Gln Ser Ile
138      50                  55                  60
140 Asn Trp Leu Arg Asp Gly Val Gln Leu Val Glu Ser Asn Arg Thr Arg
141  65                  70                  75                  80
143 Ile Thr Gly Glu Glu Val Glu Val Arg Asp Ser Ile Pro Ala Asp Ser
144                  85                  90                  95
146 Gly Leu Tyr Ala Cys Val Thr Ser Ser Pro Ser Gly Ser Asp Thr Thr
```

RAW SEQUENCE LISTING DATE: 01/25/2001
PATENT APPLICATION: US/09/757,415 TIME: 11:32:38

Input Set : A:\2459002n.app
Output Set: N:\CRF3\01252001\I757415.raw

```
147                 100                 105                 110
149 Tyr Phe Ser Val Asn Val Ser Asp Ala Leu Pro Ser Ser Glu Asp Asp
150         115                 120                 125
152 Asp Asp Asp Asp Asp Ser Ser Ser Glu Glu Lys Glu Thr Asp Asn Thr
153     130                 135                 140
155 Lys Pro Asn Arg Arg Pro Val Ala Pro Tyr Trp Thr Ser Pro Glu Lys
156 145                 150                 155                 160
158 Met Glu Lys Lys Leu His Ala Val Pro Ala Ala Lys Thr Val Lys Phe
159                 165                 170                 175
161 Lys Cys Pro Ser Ser Gly Thr Pro Asn Pro Thr Leu Arg Trp Leu Lys
162             180                 185                 190
164 Asn Gly Lys Glu Phe Lys Pro Asp His Arg Ile Gly Gly Tyr Lys Val
165         195                 200                 205
167 Arg Tyr Ala Thr Trp Ser Ile Ile Met Asp Ser Val Val Pro Ser Asp
168     210                 215                 220
170 Lys Gly Asn Tyr Thr Cys Ile Val Glu Asn Glu Tyr Gly Ser Ile Asn
171 225                 230                 235                 240
173 His Thr Tyr Gln Leu Asp Val Val Glu Arg Ser Pro His Arg Pro Ile
174                 245                 250                 255
176 Leu Gln Ala Gly Leu Pro Ala Asn Glu Thr Val Ala Leu Gly Ser Asn
177             260                 265                 270
179 Val Glu Phe Met Cys Lys Val Tyr Ser Asp Pro Gln Pro His Ile Gln
180         275                 280                 285
182 Trp Leu Lys His Ile Glu Val Asn Gly Ser Lys Ile Gly Pro Asp Asn
183     290                 295                 300
185 Leu Pro Tyr Val Gln Ile Leu Lys Thr Ala Gly Val Asn Thr Thr Asp
186 305                 310                 315                 320
188 Lys Glu Met Glu Val Leu His Leu Arg Asn Val Ser Phe Glu Asp Ala
189                 325                 330                 335
191 Gly Glu Tyr Thr Cys Leu Ala Gly Asn Ser Ile Gly Leu Ser His His
192             340                 345                 350
194 Ser Ala Trp Leu Thr Val Leu Glu Ala Leu Glu Glu Arg Pro Ala Val
195         355                 360                 365
197 Met Thr Ser Pro Leu Tyr Leu Glu Ile Ile Ile Tyr Cys Thr Gly Ala
198     370                 375                 380
200 Phe Leu Ile Ser Cys Met Leu Gly Ser Val Ile Ile Tyr Lys Met Lys
201 385                 390                 395                 400
203 Ser Gly Thr Lys Lys Ser Asp Phe His Ser Gln Met Ala Val His Lys
204                 405                 410                 415
206 Leu Ala Lys Ser Ile Pro Leu Arg Arg Gln Val Thr Val Ser Ala Asp
207             420                 425                 430
209 Ser Ser Ala Ser Met Asn Ser Gly Val Leu Leu Val Arg Pro Ser Arg
210         435                 440                 445
212 Leu Ser Ser Ser Gly Thr Pro Met Pro Ala Gly Val Ser Glu Tyr Glu
213     450                 455                 460
215 Leu Pro Glu Asp Pro Arg Trp Glu Leu Pro Arg Asp Arg Leu Val Leu
216 465                 470                 475                 480
218 Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val Val Leu Ala Glu
219                 485                 490                 495
```

RAW SEQUENCE LISTING DATE: 01/25/2001
PATENT APPLICATION: US/09/757,415 TIME: 11:32:38

Input Set : A:\2459002n.app
Output Set: N:\CRF3\01252001\I757415.raw

```
221 Ala Ile Gly Leu Asp Lys Asp Lys Pro Asn Arg Val Thr Lys Val Ala
222             500                 505                 510
224 Val Lys Met Leu Lys Ser Asp Ala Thr Glu Lys Asp Leu Ser Asp Leu
225         515                 520                 525
227 Ile Ser Glu Met Glu Met Met Lys Met Ile Gly Lys His Lys Asn Ile
228     530                 535                 540
230 Ile Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro Leu Tyr Val Ile
231 545                 550                 555                 560
233 Val Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr Leu Gln Ala Arg
234                 565                 570                 575
236 Arg Pro Pro Gly Leu Glu Tyr Cys Tyr Asn Pro Ser His Asn Pro Glu
237             580                 585                 590
239 Glu Gln Leu Ser Ser Lys Asp Leu Val Ser Cys Ala Tyr Gln Val Ala
240         595                 600                 605
242 Arg Gly Met Glu Tyr Leu Ala Ser Lys Lys Cys Ile His Arg Asp Leu
243     610                 615                 620
245 Ala Ala Arg Asn Val Leu Val Thr Glu Asp Asn Val Met Lys Ile Ala
246 625                 630                 635                 640
248 Asp Phe Gly Leu Ala Arg Asp Ile His His Ile Asp Tyr Tyr Lys Lys
249                 645                 650                 655
251 Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala Pro Glu Ala Leu
252             660                 665                 670
254 Phe Asp Arg Ile Tyr Thr His Gln Ser Asp Val Trp Ser Phe Gly Val
255         675                 680                 685
257 Leu Leu Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro Tyr Pro Gly Val
258     690                 695                 700
260 Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly His Arg Met Asp
261 705                 710                 715                 720
263 Lys Pro Ser Asn Cys Thr Asn Glu Leu Tyr Met Met Met Arg Asp Cys
264                 725                 730                 735
266 Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys Gln Leu Val Glu
267             740                 745                 750
269 Asp Leu Asp Arg Ile Val Ala Leu Thr Ser Ser Gln Glu Tyr Leu Asp
270         755                 760                 765
272 Leu Ser Ile Pro Leu Asp Gln Tyr Ser Pro Ser Phe Pro Asp Thr Arg
273     770                 775                 780
275 Ser Ser Thr Cys Ser Ser Gly Glu Asp Ser Val Phe Ser His Glu Pro
276 785                 790                 795                 800
278 Leu Pro Glu Glu Pro Cys Leu Pro Arg His Pro Thr Gln Leu Ala Asn
279                 805                 810                 815
281 Ser Gly Leu Lys Arg Arg
282             820
285 <210> SEQ ID NO: 3
286 <211> LENGTH: 22
287 <212> TYPE: PRT
288 <213> ORGANISM: Mouse
290 <400> SEQUENCE: 3
291 His Ser Gln Met Ala Val His Lys Leu Ala Lys Ser Ile Pro Leu Arg
292   1               5                  10                  15
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RAW SEQUENCE LISTING DATE: 01/25/2001
PATENT APPLICATION: US/09/757,415 TIME: 11:32:38

Input Set : A:\2459002n.app
Output Set: N:\CRF3\01252001\I757415.raw

294 Arg Gln Val Thr Val Ser
295 20
298 <210> SEQ ID NO: 4
299 <211> LENGTH: 11
300 <212> TYPE: PRT
301 <213> ORGANISM: Artificial Sequence
303 <220> FEATURE:
304 <223> OTHER INFORMATION: Description of Artificial Sequence:
305 tyrosine-phosphorylated peptide
307 <220> FEATURE:
308 <223> OTHER INFORMATION: X = phosphotyrosine
310 <400> SEQUENCE: 4
W--> **311 Leu Val Ile Ala Gly Asn Pro Ala Xaa Arg Ser**
312 1 5 10
315 <210> SEQ ID NO: 5
316 <211> LENGTH: 16
317 <212> TYPE: PRT
318 <213> ORGANISM: Artificial Sequence
320 <220> FEATURE:
321 <223> OTHER INFORMATION: Description of Artificial Sequence: consensus
323 <220> FEATURE:
324 <223> OTHER INFORMATION: Xaa can be any amino acid
326 <400> SEQUENCE: 5
W--> **327 Val Xaa Xaa Leu Xaa Xaa Xaa Ile Xaa Leu Xaa Arg Xaa Val Xaa Val**
328 1 5 10 15
331 <210> SEQ ID NO: 6
332 <211> LENGTH: 4
333 <212> TYPE: PRT
334 <213> ORGANISM: Artificial Sequence
336 <220> FEATURE:
337 <223> OTHER INFORMATION: Description of Artificial Sequence: motif
339 <220> FEATURE:
340 <223> OTHER INFORMATION: X in the 3rd position= any amino acid
342 <220> FEATURE:
343 <223> OTHER INFORMATION: X in the 4th position= phosphotyrosine
345 <400> SEQUENCE: 6
W--> **346 Asn Pro Xaa Xaa**
347 1
350 <210> SEQ ID NO: 7
351 <211> LENGTH: 12
352 <212> TYPE: PRT
353 <213> ORGANISM: Artificial Sequence
355 <220> FEATURE:
356 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
357 peptide derived from TrkA receptor
359 <400> SEQUENCE: 7
W--> **360 His Ile Ile Glu Asn Pro Gln Xaa Phe Ser Asp Ala**
361 1 5 10

see item 10 on Error Summary Sheet

VERIFICATION SUMMARY DATE: 01/25/2001
PATENT APPLICATION: US/09/757,415 TIME: 11:32:39

Input Set : A:\2459002n.app
Output Set: N:\CRF3\01252001\I757415.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:311 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:311 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:311 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:4
L:327 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:327 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:327 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:5
L:346 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:346 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:346 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6
L:360 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7
L:360 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7
L:360 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:7